



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:23 PM UTC

PDB ID : 2R16 / pdb_00002r16
Title : Crystal Structure of bovine neuexin 1 alpha LNS/LG domain 4 (with no splice insert)
Authors : Rudenko, G.
Deposited on : 2007-08-22
Resolution : 1.04 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

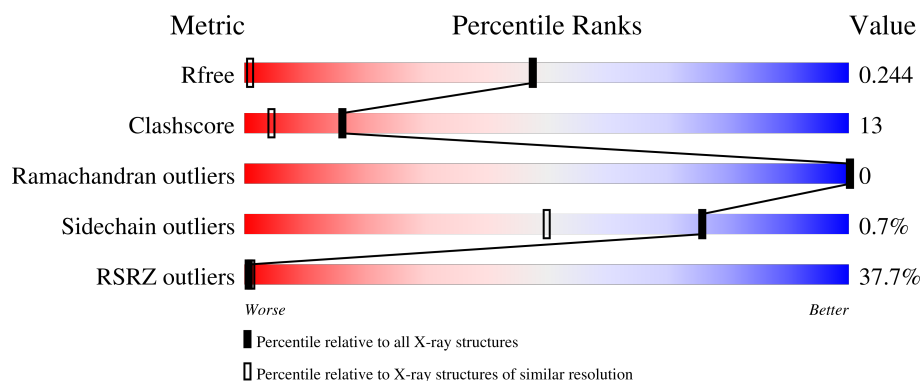
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.04 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1036 (1.06-1.02)
Clashscore	190562	1063 (1.06-1.02)
Ramachandran outliers	187476	1034 (1.06-1.02)
Sidechain outliers	187428	1035 (1.06-1.02)
RSRZ outliers	180081	1035 (1.06-1.02)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	182	36% 78% 18% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1607 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Neurexin-1-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	0	23	0
			1476	924	257	281	14			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	719	GLY	-	expression tag	UNP Q28146
A	720	SER	-	expression tag	UNP Q28146
A	?	-	ASP	deletion	UNP Q28146
A	?	-	CYS	deletion	UNP Q28146
A	?	-	ILE	deletion	UNP Q28146
A	?	-	ARG	deletion	UNP Q28146
A	?	-	ILE	deletion	UNP Q28146
A	?	-	ASN	deletion	UNP Q28146
A	?	-	CYS	deletion	UNP Q28146
A	?	-	ASN	deletion	UNP Q28146
A	?	-	SER	deletion	UNP Q28146
A	790	GLY	SER	expression tag	UNP Q28146

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

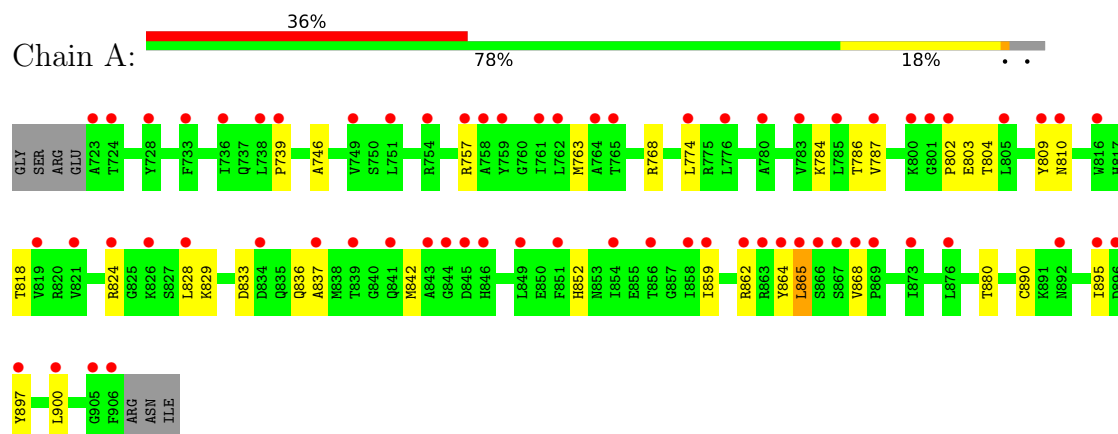
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	130	Total	O	0	0
			130	130		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Neurexin-1-alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	90.32Å 90.32Å 39.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	23.70 – 1.04 23.70 – 1.04	Depositor EDS
% Data completeness (in resolution range)	100.0 (23.70-1.04) 91.3 (23.70-1.04)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.17 (at 1.04Å)	Xtriage
Refinement program	REFMAC 5.3, CNS	Depositor
R, R_{free}	0.146 , 0.165 0.235 , 0.244	Depositor DCC
R_{free} test set	8108 reflections (10.03%)	wwPDB-VP
Wilson B-factor (Å ²)	9.1	Xtriage
Anisotropy	0.141	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1607	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.78	2/1558 (0.1%)	0.84	0/2100

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	865	LEU	N-CA	-5.70	1.39	1.46
1	A	864	TYR	CA-C	-5.59	1.44	1.52

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1476	0	1455	39	0
2	A	1	0	0	0	0
3	A	130	0	0	6	0
All	All	1607	0	1455	39	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (39) close contacts within the same asymmetric unit are listed below, sorted by their clash

magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:803[B]:GLU:HG2	1:A:842[B]:MET:CE	1.65	1.26
1:A:803[B]:GLU:CG	1:A:842[B]:MET:HE1	1.70	1.22
1:A:803[B]:GLU:CD	1:A:842[B]:MET:HE3	1.67	1.19
1:A:803[B]:GLU:CG	1:A:842[B]:MET:CE	2.31	1.06
1:A:803[B]:GLU:CD	1:A:842[B]:MET:CE	2.34	1.00
1:A:890[B]:CYS:SG	1:A:900:LEU:CD2	2.54	0.95
1:A:890[B]:CYS:SG	1:A:900:LEU:HD23	2.08	0.94
1:A:862:ARG:NH1	1:A:868:VAL:HG13	1.97	0.80
1:A:768:ARG:H	1:A:852:HIS:HD2	1.32	0.78
1:A:774[A]:LEU:HD12	1:A:787:VAL:HG22	1.66	0.77
1:A:803[B]:GLU:HG2	1:A:842[B]:MET:HE1	0.83	0.75
1:A:818[B]:THR:HG22	1:A:833:ASP:HA	1.67	0.74
1:A:768:ARG:H	1:A:852:HIS:CD2	2.08	0.71
1:A:774[A]:LEU:CD1	1:A:787:VAL:HG22	2.22	0.70
1:A:786:THR:HG21	3:A:1109:HOH:O	1.93	0.68
1:A:803[B]:GLU:OE2	1:A:842[B]:MET:HE3	1.99	0.63
1:A:802:PRO:HB3	3:A:1090:HOH:O	2.00	0.61
1:A:862:ARG:O	1:A:865:LEU:HB3	2.05	0.56
1:A:746:ALA:HB1	1:A:824:ARG:HE	1.70	0.55
1:A:862:ARG:HH12	1:A:868:VAL:HG13	1.71	0.54
1:A:809:TYR:HD1	1:A:810:ASN:ND2	2.09	0.50
1:A:836[B]:GLN:HG2	1:A:836[B]:GLN:O	2.11	0.50
1:A:836[B]:GLN:O	1:A:836[B]:GLN:CG	2.57	0.49
1:A:890[B]:CYS:SG	1:A:900:LEU:HD21	2.49	0.48
1:A:818[B]:THR:HG23	3:A:1014:HOH:O	2.13	0.48
1:A:895:ILE:HB	1:A:897[B]:TYR:CE2	2.50	0.46
1:A:787:VAL:HG21	1:A:828:LEU:HD11	1.97	0.46
1:A:818[B]:THR:CG2	1:A:833:ASP:HA	2.39	0.46
1:A:784:LYS:HE3	1:A:804[B]:THR:HG21	1.97	0.45
1:A:862:ARG:O	1:A:865:LEU:CB	2.65	0.45
1:A:852:HIS:HE1	3:A:1101:HOH:O	1.99	0.44
1:A:880[B]:THR:HG22	3:A:1098:HOH:O	2.17	0.44
1:A:862:ARG:HA	1:A:865:LEU:HB2	2.02	0.42
1:A:862:ARG:NH2	3:A:1087:HOH:O	2.51	0.41
1:A:829:LYS:CG	1:A:837:ALA:HB1	2.51	0.41
1:A:859:ILE:O	1:A:862:ARG:CZ	2.69	0.41
1:A:739:PRO:HD3	1:A:897[A]:TYR:CE1	2.56	0.40
1:A:895:ILE:HD12	1:A:897[B]:TYR:CE1	2.55	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	196/182 (108%)	194 (99%)	2 (1%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	169/156 (108%)	168 (99%)	1 (1%)	78	52

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	757	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	743	HIS
1	A	810	ASN
1	A	852	HIS
1	A	892	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	175/182 (96%)	1.92	66 (37%) 1 1	6, 13, 20, 25	23 (13%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	906	PHE	12.4
1	A	723	ALA	9.6
1	A	809	TYR	6.6
1	A	843	ALA	5.6
1	A	865	LEU	4.9
1	A	810	ASN	4.4
1	A	867	SER	4.2
1	A	845	ASP	4.1
1	A	905	GLY	3.9
1	A	866	SER	3.9
1	A	739	PRO	3.7
1	A	828	LEU	3.6
1	A	868	VAL	3.5
1	A	896	ASP	3.5
1	A	802	PRO	3.4
1	A	862	ARG	3.4
1	A	897[A]	TYR	3.3
1	A	724	THR	3.3
1	A	774[A]	LEU	3.3
1	A	821[A]	VAL	3.3
1	A	764	ALA	3.2
1	A	863	ARG	3.1
1	A	846	HIS	3.1
1	A	858	ILE	3.0
1	A	837	ALA	3.0
1	A	816	TRP	3.0
1	A	824	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	844	GLY	2.9
1	A	841	GLN	2.8
1	A	736	ILE	2.8
1	A	854	ILE	2.8
1	A	780	ALA	2.8
1	A	800[A]	LYS	2.8
1	A	762	LEU	2.8
1	A	761	ILE	2.7
1	A	733	PHE	2.7
1	A	801[A]	GLY	2.6
1	A	776	LEU	2.6
1	A	834	ASP	2.6
1	A	738	LEU	2.5
1	A	839	THR	2.5
1	A	849	LEU	2.5
1	A	856	THR	2.4
1	A	864	TYR	2.4
1	A	759	TYR	2.4
1	A	749	VAL	2.4
1	A	765	THR	2.3
1	A	805	LEU	2.3
1	A	892	ASN	2.2
1	A	859	ILE	2.2
1	A	873	ILE	2.2
1	A	751[A]	LEU	2.2
1	A	785	LEU	2.2
1	A	728	TYR	2.2
1	A	826	LYS	2.2
1	A	787	VAL	2.1
1	A	869	PRO	2.1
1	A	754	ARG	2.1
1	A	783	VAL	2.1
1	A	819	VAL	2.1
1	A	851	PHE	2.0
1	A	900	LEU	2.0
1	A	895	ILE	2.0
1	A	757	ARG	2.0
1	A	758	ALA	2.0
1	A	876	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	CA	A	1000	1/1	0.99	0.04	6,6,6,6	1

6.5 Other polymers [i](#)

There are no such residues in this entry.